

06870090-053001

EXPRESS MAIL NO. EL 446402222US

PC9979ASequence.txt

gct ggc cca ggc gat ggg cga cca aat ctg cgc atg aag ttc cag ggc 3
 03
 Ala Gly Pro Gly Asp Gly Arg Pro Asn Leu Arg Met Lys Phe Gln Gly
 60 65 70

gcc ttc cgc aag ggg gtg ccc aac ccc atc gat ctg ctg gag tcc acc 3
 51
 Ala Phe Arg Lys Gly Val Pro Asn Pro Ile Asp Leu Leu Glu Ser Thr
 75 80 85

cta tat gag tcc tgg gtg gtg cct ggg ccc aag aaa gca ccc atg gac 3
 99
 Leu Tyr Glu Ser Ser Val Val Pro Gly Pro Lys Lys Ala Pro Met Asp
 90 95 100 105

tca ctg ttt gac tac ggc acc tat cgt cac cac tcc agt gac aac aag 4
 47
 Ser Leu Phe Asp Tyr Gly Thr Tyr Arg His His Ser Ser Asp Asn Lys
 110 115 120

agg tgg agg aag aag atc ata gag aag cag ccg cag agc ccc aaa gcc 4
 95
 Arg Trp Arg Lys Lys Ile Ile Glu Lys Gln Pro Gln Ser Pro Lys Ala
 125 130 135

cct gcc cct cag ccg ccc ccc atc ctc aaa gtc ttc aac cgg cct atc 5
 43
 Pro Ala Pro Gln Pro Pro Pro Ile Leu Lys Val Phe Asn Arg Pro Ile
 140 145 150

ctc ttt gac atc gtg tcc cgg ggc tcc act gct gac ctg gac ggg ctg 5
 91
 Leu Phe Asp Ile Val Ser Arg Gly Ser Thr Ala Asp Leu Asp Gly Leu
 155 160 165

ctc cca ttc ttg ctg acc cac aag aaa cgc cta act gat gag gag ttt 6
 39
 Leu Pro Phe Leu Leu Thr His Lys Lys Arg Leu Thr Asp Glu Glu Phe
 170 175 180 185

cga gag cca tct acg ggg aag acc tgc ctg ccc aag gcc ttg ctg aac 6
 87
 Arg Glu Pro Ser Thr Gly Lys Thr Cys Leu Pro Lys Ala Leu Leu Asn
 190 195 200

ctg agc aat ggc cgc aac gac acc atc cct gtg ctg ctg gac atc gcg 7
 35
 Leu Ser Asn Gly Arg Asn Asp Thr Ile Pro Val Leu Leu Asp Ile Ala
 205 210 215

gag cgc acc ggc aac atg cgg gag ttc att aac tgg ccc ttc cgt gac 7
 83

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 A2
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PC9979ASequence.txt

Glu	Arg	Thr	Gly	Asn	Met	Arg	Glu	Phe	Ile	Asn	Ser	Pro	Phe	Arg	Asp		
	220						225					230					
atc	tac	tat	cga	ggt	cag	aca	gcc	ctg	cac	atc	gcc	att	gag	cgt	cgc	8	
31																	
Ile	Tyr	Tyr	Arg	Gly	Gln	Thr	Ala	Leu	His	Ile	Ala	Ile	Glu	Arg	Arg		
	235					240					245						
tgc	aaa	cac	tac	gtg	gaa	ctt	ctc	gtg	gcc	cag	gga	gct	gat	gtc	cac	8	
79																	
Cys	Lys	His	Tyr	Val	Glu	Leu	Leu	Val	Ala	Gln	Gly	Ala	Asp	Val	His		
250					255					260					265		
gcc	cag	gcc	cgt	ggg	cgc	ttc	ttc	cag	ccc	aag	gat	gag	ggg	ggc	tac	9	
27																	
Ala	Gln	Ala	Arg	Gly	Arg	Phe	Phe	Gln	Pro	Lys	Asp	Glu	Gly	Gly	Tyr		
				270					275						280		
ttc	tac	ttt	ggg	gag	ctg	ccc	ctg	tcg	ctg	gct	gcc	tgc	acc	aac	cag	9	
75																	
Phe	Tyr	Phe	Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Asn	Gln		
			285					290					295				
ccc	cac	att	gtc	aac	tac	cta	acg	gag	aac	ccc	cac	aag	aag	gcg	gac	1	
023																	
Pro	His	Ile	Val	Asn	Tyr	Leu	Thr	Glu	Asn	Pro	His	Lys	Lys	Ala	Asp		
		300					305					310					
atg	cgg	cgc	cag	gac	tcg	cga	ggc	aac	aca	gtg	ctg	cat	gcg	ctg	gtg	1	
071																	
Met	Arg	Arg	Gln	Asp	Ser	Arg	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val		
	315					320					325						
gcc	att	gct	gac	aac	acc	cgt	gag	aac	acc	aag	ttt	gtt	acc	aag	atg	1	
119																	
Ala	Ile	Ala	Asp	Asn	Thr	Arg	Glu	Asn	Thr	Lys	Phe	Val	Thr	Lys	Met		
330					335					340					345		
tac	gac	ctg	ctg	ctg	ctc	aag	tgt	gcc	cgc	ctc	ttc	ccc	gac	agc	aac	1	
167																	
Tyr	Asp	Leu	Leu	Leu	Leu	Lys	Cys	Ala	Arg	Leu	Phe	Pro	Asp	Ser	Asn		
				350					355					360			
ctg	gag	gcc	gtg	ctc	aac	aac	gac	ggc	ctc	tcg	ccc	ctc	atg	atg	gct	1	
215																	
Leu	Glu	Ala	Val	Leu	Asn	Asn	Asp	Gly	Leu	Ser	Pro	Leu	Met	Met	Ala		
			365					370					375				
gcc	aag	acg	ggc	aag	att	ggg	atc	ttt	cag	cac	atc	atc	cgg	cgg	gag	1	
263																	
Ala	Lys	Thr	Gly	Lys	Ile	Gly	Ile	Phe	Gln	His	Ile	Ile	Arg	Arg	Glu		
		380					385					390					

T00050" 06002860

1000
 1000
 1000

PC9979ASequence.txt

gtg acg gat gag gac aca cgg cac ctg tcc cgc aag ttc aag gac tgg 1
311
Val Thr Asp Glu Asp Thr Arg His Leu Ser Arg Lys Phe Lys Asp Trp
395 400 405

gcc tat ggg cca gtg tat tcc tcg ctt tat gac ctc tcc tcc ctg gac 1
359
Ala Tyr Gly Pro Val Tyr Ser Ser Leu Tyr Asp Leu Ser Ser Leu Asp
410 415 420 425

acg tgt ggg gaa gag gcc tcc gtg ctg gag atc ctg gtg tac aac agc 1
407
Thr Cys Gly Glu Glu Ala Ser Val Leu Glu Ile Leu Val Tyr Asn Ser
430 435 440

aag att gag aac cgc cac gag atg ctg gct gtg gag ccc atc aat gaa 1
455
Lys Ile Glu Asn Arg His Glu Met Leu Ala Val Glu Pro Ile Asn Glu
445 450 455

ctg ctg cgg gac aag tgg cgc aag ttc ggg gcc gtc tcc ttc tac atc 1
503
Leu Leu Arg Asp Lys Trp Arg Lys Phe Gly Ala Val Ser Phe Tyr Ile
460 465 470

aac gtg gtc tcc tac ctg tgt gcc atg gtc atc ttc act ctc acc gcc 1
551
Asn Val Val Ser Tyr Leu Cys Ala Met Val Ile Phe Thr Leu Thr Ala
475 480 485

tac tac cag ccg ctg gag ggc aca ccg ccg tac cct tac cgc acc acg 1
599
Tyr Tyr Gln Pro Leu Glu Gly Thr Pro Pro Tyr Pro Tyr Arg Thr Thr
490 495 500 505

gtg gac tac ctg cgg ctg gct ggc gag gtc att acg ctc ttc act ggg 1
647
Val Asp Tyr Leu Arg Leu Ala Gly Glu Val Ile Thr Leu Phe Thr Gly
510 515 520

gtc ctg ttc ttc ttc acc aac atc aaa gac ttg ttc atg aag aaa tgc 1
695
Val Leu Phe Phe Phe Thr Asn Ile Lys Asp Leu Phe Met Lys Lys Cys
525 530 535

cct gga gtg aat tct ctc ttc att gat ggc tcc ttc cag ctg ctc tac 1
743
Pro Gly Val Asn Ser Leu Phe Ile Asp Gly Ser Phe Gln Leu Leu Tyr
540 545 550

ttc atc tac tct gtc ctg gtg atc gtc tca gca gcc ctc tac ctg gca 1

Sub
A2
Cmt

e	Tyr	Ser	Val	Leu	Val	Ile	Val	Ser	Ala	Ala
5					560					565
c	gag	gcc	tac	ctg	gcc	gtg	atg	gtc	ttt	gcc
e	Glu	Ala	Tyr	Leu	Ala	Val	Met	Val	Phe	Ala
				575					580	
g	aat	gcc	ctt	tac	ttc	acc	cgt	ggg	ctg	aag
t	Asn	Ala	Leu	Tyr	Phe	Thr	Arg	Gly	Leu	Lys
			590					595		
c	atc	atg	atc	cag	aag	att	ctc	ttc	aag	gac
r	Ile	Met	Ile	Gln	Lys	Ile	Leu	Phe	Lys	Asp
		605					610			
c	gtc	tac	ttg	ctc	ttc	atg	atc	ggc	tac	gct
u	Val	Tyr	Leu	Leu	Phe	Met	Ile	Gly	Tyr	Ala
	620					625				
c	ctg	aac	ccg	tgt	goc	aac	atg	aag	gtg	tgc
u	Leu	Asn	Pro	Cys	Ala	Asn	Met	Lys	Val	Cys
5					640					645
c	tgc	aca	gtg	ccc	act	tac	ccc	tcg	tgc	cgt
n	Cys	Thr	Val	Pro	Thr	Tyr	Pro	Ser	Cys	Arg
				655					660	
c	acc	ttc	ctc	ctg	gac	ctg	ttt	aag	ctg	acc
r	Thr	Phe	Leu	Leu	Asp	Leu	Phe	Lys	Leu	Thr
			670					675		
g	gag	atg	ctg	agc	agc	acc	aag	tac	ccc	gtg
u	Glu	Met	Leu	Ser	Ser	Thr	Lys	Tyr	Pro	Val
		685					690			
g	gtg	acc	tac	atc	atc	ctc	acc	ttt	gtg	ctg
u	Val	Thr	Tyr	Ile	Ile	Leu	Thr	Phe	Val	Leu
	700					705				
t	gcc	ctc	atg	ggc	gag	aca	gtg	ggc	cag	gtc
e	Ala	Leu	Met	Gly	Glu	Thr	Val	Gly	Gln	Val

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Sub
a2
cont

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

PC9979ASequence.txt

715

720

725

aag cac atc tgg aag ctg cag tgg gcc acc acc atc ctg gac att gag 2
319

Lys His Ile Trp Lys Leu Gln Trp Ala Thr Thr Ile Leu Asp Ile Glu
730 735 740 745

cgc tcc ttc ccc gta ttc ctg agg aag gcc ttc cgc tct ggg gag atg 2
367

Arg Ser Phe Pro Val Phe Leu Arg Lys Ala Phe Arg Ser Gly Glu Met
750 755 760

gtc acc gtg ggc aag agc tcg gac ggc act cct gac cgc agg tgg tgc 2
415

Val Thr Val Gly Lys Ser Ser Asp Gly Thr Pro Asp Arg Arg Trp Cys
765 770 775

ttc agg gtg gat gag gtg aac tgg tct cac tgg aac cag aac ttg ggc 2
463

Phe Arg Val Asp Glu Val Asn Trp Ser His Trp Asn Gln Asn Leu Gly
780 785 790

atc atc aac gag gac ccg ggc aag aat gag acc tac cag tat tat ggc 2
511

Ile Ile Asn Glu Asp Pro Gly Lys Asn Glu Thr Tyr Gln Tyr Tyr Gly
795 800 805

ttc tcg cat acc gtg ggc cgc ctc cgc agg gat cgc tgg tcc tcg gtg 2
559

Phe Ser His Thr Val Gly Arg Leu Arg Arg Asp Arg Trp Ser Ser Val
810 815 820 825

gta ccc cgc gtg gtg gaa ctg aac aag aac tcg aac ccg gac gag gtg 2
607

Val Pro Arg Val Val Glu Leu Asn Lys Asn Ser Asn Pro Asp Glu Val
830 835 840

gtg gtg cct ctg gac agc atg ggg aac ccc cgc tgc gat ggc cac cag 2
655

Val Val Pro Leu Asp Ser Met Gly Asn Pro Arg Cys Asp Gly His Gln
845 850 855

cag ggt tac ccc cgc aag tgg agg act gat gac gcc ccg ctc tag 2
700

Gln Gly Tyr Pro Arg Lys Trp Arg Thr Asp Asp Ala Pro Leu
860 865 870

ggactgcagc ccagccccag cttctctgcc cactcatttc tagtccagc 2
749

<210> 2

T00250" 05002850

Sub
A2
Cont

PC9979ASequence.txt

<211> 871

<212> PRT

<213> Human

<400> 2

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Leu Ser Ser Leu Ala Asn Leu Phe Glu Gly Glu Asp Gly Ser Leu Ser
35 40 45
Pro Ser Pro Ala Asp Ala Ser Arg Pro Ala Gly Pro Gly Asp Gly Arg
50 55 60
Pro Asn Leu Arg Met Lys Phe Gln Gly Ala Phe Arg Lys Gly Val Pro
65 70 75 80
Asn Pro Ile Asp Leu Leu Glu Ser Thr Leu Tyr Glu Ser Ser Val Val
85 90 95
Pro Gly Pro Lys Lys Ala Pro Met Asp Ser Leu Phe Asp Tyr Gly Thr
100 105 110
Tyr Arg His His Ser Ser Asp Asn Lys Arg Trp Arg Lys Lys Ile Ile
115 120 125
Glu Lys Gln Pro Gln Ser Pro Lys Ala Pro Ala Pro Gln Pro Pro Pro
130 135 140
Ile Leu Lys Val Phe Asn Arg Pro Ile Leu Phe Asp Ile Val Ser Arg
145 150 155 160
Gly Ser Thr Ala Asp Leu Asp Gly Leu Leu Pro Phe Leu Leu Thr His
165 170 175
Lys Lys Arg Leu Thr Asp Glu Glu Phe Arg Glu Pro Ser Thr Gly Lys
180 185 190
Thr Cys Leu Pro Lys Ala Leu Leu Asn Ile Ala Glu Arg Thr Gly Asn Met Arg
195 200 205
Thr Ile Pro Val Leu Leu Asp Ile Ala Glu Arg Thr Gly Asn Met Arg
210 215 220
Glu Phe Ile Asn Ser Pro Phe Arg Asp Ile Tyr Tyr Arg Gly Gln Thr
225 230 235 240
Ala Leu His Ile Ala Ile Glu Arg Arg Cys Lys His Tyr Val Glu Leu
245 250 255
Leu Val Ala Gln Gly Ala Asp Val His Ala Gln Ala Arg Gly Arg Phe
260 265 270
Phe Gln Pro Lys Asp Glu Gly Gly Tyr Phe Tyr Phe Gly Glu Leu Pro
275 280 285
Leu Ser Leu Ala Ala Cys Thr Asn Gln Pro His Ile Val Asn Tyr Leu
290 295 300
Thr Glu Asn Pro His Lys Lys Ala Asp Met Arg Arg Gln Asp Ser Arg
305 310 315 320
Gly Asn Thr Val Leu His Ala Leu Val Ala Ile Ala Asp Asn Thr Arg
325 330 335
Glu Asn Thr Lys Phe Val Thr Lys Met Tyr Asp Leu Leu Leu Lys
340 345 350
Cys Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val Leu Asn Asn
355 360 365
Asp Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly Lys Ile Gly

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CNC

PC9979ASequence.txt

370 375 380
 Ile Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu Asp Thr Arg
 385 390 395 400
 His Leu Ser Arg Lys Phe Lys Asp Trp Ala Tyr Gly Pro Val Tyr Ser
 405 410 415
 Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu Glu Ala Ser
 420 425 430
 Val Leu Glu Ile Leu Val Tyr Asn Ser Lys Ile Glu Asn Arg His Glu
 435 440 445
 Met Leu Ala Val Glu Pro Ile Asn Glu Leu Leu Arg Asp Lys Trp Arg
 450 455 460
 Lys Phe Gly Ala Val Ser Phe Tyr Ile Asn Val Val Ser Tyr Leu Cys
 465 470 475 480
 Ala Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro Leu Glu Gly
 485 490 495
 Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu Arg Leu Ala
 500 505 510
 Gly Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe Phe Thr Asn
 515 520 525
 Ile Lys Asp Leu Phe Met Lys Lys Cys Pro Gly Val Asn Ser Leu Phe
 530 535 540
 Ile Asp Gly Ser Phe Gln Leu Leu Tyr Phe Ile Tyr Ser Val Leu Val
 545 550 555 560
 Ile Val Ser Ala Ala Leu Tyr Leu Ala Gly Ile Glu Ala Tyr Leu Ala
 565 570 575
 Val Met Val Phe Ala Leu Val Leu Gly Trp Met Asn Ala Leu Tyr Phe
 580 585 590
 Thr Arg Gly Leu Lys Leu Thr Gly Thr Tyr Ser Ile Met Ile Gln Lys
 595 600 605
 Ile Leu Phe Lys Asp Leu Phe Arg Phe Leu Leu Val Tyr Leu Leu Phe
 610 615 620
 Met Ile Gly Tyr Ala Ser Ala Leu Val Ser Leu Leu Asn Pro Cys Ala
 625 630 635 640
 Asn Met Lys Val Cys Asn Glu Asp Gln Thr Asn Cys Thr Val Pro Thr
 645 650 655
 Tyr Pro Ser Cys Arg Asp Ser Glu Thr Phe Ser Thr Phe Leu Leu Asp
 660 665 670
 Leu Phe Lys Leu Thr Ile Gly Met Gly Asp Leu Glu Met Leu Ser Ser
 675 680 685
 Thr Lys Tyr Pro Val Val Phe Ile Ile Leu Leu Val Thr Tyr Ile Ile
 690 695 700
 Leu Thr Phe Val Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu
 705 710 715 720
 Thr Val Gly Gln Val Ser Lys Glu Ser Lys His Ile Trp Lys Leu Gln
 725 730 735
 Trp Ala Thr Thr Ile Leu Asp Ile Glu Arg Ser Phe Pro Val Phe Leu
 740 745 750
 Arg Lys Ala Phe Arg Ser Gly Glu Met Val Thr Val Gly Lys Ser Ser
 755 760 765
 Asp Gly Thr Pro Asp Arg Arg Trp Cys Phe Arg Val Asp Glu Val Asn
 770 775 780
 Trp Ser His Trp Asn Gln Asn Leu Gly Ile Ile Asn Glu Asp Pro Gly

T00050" 06002860

Sub
 A2
 comp

09070090-053001

<210>	3
<211>	1900
<212>	DNA
<213>	Human

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att aac tgc ccc ttc cgt gac atc / tac tat cga ggg gag ctg ccc ctg 1
02

tcg ctg gct gcc tgc acc aac cag ccc cac att gtc aac tac ctg acg 1
50

gag aac ccc cac aag aag gcg gac atg ~~cg~~ cgc cag gac tcg cga ggc 1
98

aac aca gtg ctg cat gcg ctg gtg gcc att gct gac aac acc cgt gag 2
46

aac acc aag ttt gtt acc aag atg tac gac ctg ~~ctg~~ ctg ctc aag tgt 2
94

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sub
a2
cont

PC9979ASequence.txt

70

75

80

gcc cgc ctc ttc ccc gac agc aac ctg gag gcc gtg ctc aac aac gac 3
 42
 Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val Leu Asn Asn Asp
 85 90 95 100
 ggc ctc tcg ccc ctc atg atg gct gcc aag acg ggc aag att ggg atc 3
 90
 Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly Lys Ile Gly Ile
 105 110 115
 ttt cag cac atc atc cgg cgg gag gtg acg gat gag gac aca cgg cac 4
 38
 Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu Asp Thr Arg His
 120 125 130
 ctg tcc cgc aag ttc aag gac tgg gcc tat ggg cca gtg tat tcc tcg 4
 86
 Leu Ser Arg Lys Phe Lys Asp Trp Ala Tyr Gly Pro Val Tyr Ser Ser
 135 140 145
 ctt tat gac ctc tcc tcc ctg gac acg tgt ggg gaa gag gcc tcc gtg 5
 34
 Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu Glu Ala Ser Val
 150 155 160
 ctg gag atc ctg gtg tac aac agc aag att gag aac cgc cac gag atg 5
 82
 Leu Glu Ile Leu Val Tyr Asn Ser Lys Ile Glu Asn Arg His Glu Met
 165 170 175 180
 ctg gct gtg gag ccc atc aat gaa ctg ctg cgg gac aag tgg cgc aag 6
 30
 Leu Ala Val Glu Pro Ile Asn Glu Leu Leu Arg Asp Lys Trp Arg Lys
 185 190 195
 ttc ggg gcc gtc tcc ttc tac atc aac gtg gtc tcc tac ctg tgt gcc 6
 78
 Phe Gly Ala Val Ser Phe Tyr Ile Asn Val Val Ser Tyr Leu Cys Ala
 200 205 210
 atg gtc atc ttc act ctc acc gcc tac tac cag ccg ctg gag ggc aca 7
 26
 Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro Leu Glu Gly Thr
 215 220 225
 ccg ccg tac cct tac cgc acc acg gtg gac tac ctg cgg ctg gct ggc 7
 74
 Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu Arg Leu Ala Gly
 230 235 240

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 A2
 cont

PC9979ASequence.txt

gag gtc att acg ctc ttc act ggg gtc ctg ttc ttc ttc acc aac atc 8
 22
 Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe Phe Thr Asn Ile
 245 250 255 260
 aaa gac ttg ttc atg aag aaa tgc cct gga gtg aat tct ctc ttc att 8
 70
 Lys Asp Leu Phe Met Lys Lys Cys Pro Gly Val Asn Ser Leu Phe Ile
 265 270 275
 gat ggc tcc ttc cag ctg ctc tac ttc atc tac tct gtc ctg gtg atc 9
 18
 Asp Gly Ser Phe Gln Leu Leu Tyr Phe Ile Tyr Ser Val Leu Val Ile
 280 285 290
 gtc tca gca gcc ctc tac ctg gca ggg atc gag gcc tac ctg gcc gtg 9
 66
 Val Ser Ala Ala Leu Tyr Leu Ala Gly Ile Glu Ala Tyr Leu Ala Val
 295 300 305
 atg gtc ttt gcc ctg gtc ctg ggc tgg atg aat gcc ctt tac ttc acc 1
 014
 Met Val Phe Ala Leu Val Leu Gly Trp Met Asn Ala Leu Tyr Phe Thr
 310 315 320
 cgt ggg ctg aag ctg acg ggg acc tat agc atc atg atc cag aag att 1
 062
 Arg Gly Leu Lys Leu Thr Gly Thr Tyr Ser Ile Met Ile Gln Lys Ile
 325 330 335 340
 ctc ttc aag gac ctt ttc cga ttc ctg ctc gtc tac ttg ctc ttc atg 1
 110
 Leu Phe Lys Asp Leu Phe Arg Phe Leu Leu Val Tyr Leu Leu Phe Met
 345 350 355
 atc ggc tac gct tca gcc ctg gtc tcc ctc ctg aac ccg tgt gcc aac 1
 158
 Ile Gly Tyr Ala Ser Ala Leu Val Ser Leu Leu Asn Pro Cys Ala Asn
 360 365 370
 atg aag gtg tgc aat gag gac cag acc aac tgc aca gtg ccc act tac 1
 206
 Met Lys Val Cys Asn Glu Asp Gln Thr Asn Cys Thr Val Pro Thr Tyr
 375 380 385
 ccc tcg tgc cgt gac agc gag acc ttc agc acc ttc ctc ctg gac ctg 1
 254
 Pro Ser Cys Arg Asp Ser Glu Thr Phe Ser Thr Phe Leu Leu Asp Leu
 390 395 400
 ttt aag ctg acc atc ggc atg ggc gac ctg gag atg ctg agc agc acc 1
 302

See
 A2
 cont

PC9979ASequence.txt

Phe Lys Leu Thr Ile Gly Met Gly Asp Leu Glu Met Leu Ser Ser Thr
 405 410 415 420
 aag tac ccc gtg gtc ttc atc atc ctg ctg gtg acc tac atc atc ctc 1
 350
 Lys Tyr Pro Val Val Phe Ile Ile Leu Leu Val Thr Tyr Ile Ile Leu
 425 430 435
 acc ttt gtg ctg ctc ctc aac atg ctc att gcc ctc atg ggc gag aca 1
 398
 Thr Phe Val Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr
 440 445 450
 gtg ggc cag gtc tcc aag gag agc aag cac atc tgg aag ctg cag tgg 1
 446
 Val Gly Gln Val Ser Lys Glu Ser Lys His Ile Trp Lys Leu Gln Trp
 455 460 465
 gcc acc acc atc ctg gac att gag cgc tcc ttc ccc gta ttc ctg agg 1
 494
 Ala Thr Thr Ile Leu Asp Ile Glu Arg Ser Phe Pro Val Phe Leu Arg
 470 475 480
 aag gcc ttc cgc tct ggg gag atg gtc acc gtg ggc aag agc tcg gac 1
 542
 Lys Ala Phe Arg Ser Gly Glu Met Val Thr Val Gly Lys Ser Ser Asp
 485 490 495 500
 ggc act cct gac cgc agg tgg tgc ttc agg gtg gat gag gtg aac tgg 1
 590
 Gly Thr Pro Asp Arg Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp
 505 510 515
 tct cac tgg aac cag aac ttg ggc atc atc aac gag gac ccg ggc aag 1
 638
 Ser His Trp Asn Gln Asn Leu Gly Ile Ile Asn Glu Asp Pro Gly Lys
 520 525 530
 aat gag acc tac cag tat tat ggc ttc tcg cat acc gtg ggc cgc ctc 1
 686
 Asn Glu Thr Tyr Gln Tyr Tyr Gly Phe Ser His Thr Val Gly Arg Leu
 535 540 545
 cgc agg gat cgc tgg tcc tcg gtg gta ccc cgc gtg gtg gaa ctg aac 1
 734
 Arg Arg Asp Arg Trp Ser Ser Val Val Pro Arg Val Val Glu Leu Asn
 550 555 560
 aag aac tcg aac ccg gac gag gtg gtg gtg cct ctg gac agc atg ggg 1
 782
 Lys Asn Ser Asn Pro Asp Glu Val Val Val Pro Leu Asp Ser Met Gly
 565 570 575 580

T00050" 05002850

Sub
 As
 Cont

PC9979ASequence.txt

aac ccc cgc tgc gat ggc cac cag cag ggt tac ccc cgc aag tgg agg 1
 830
 Asn Pro Arg Cys Asp Gly His Gln Gln Gly Tyr Pro Arg Lys Trp Arg
 585 590 595

act gat gac gcc ccg ctc tag ggactgcagc ccagccccag cttctctgcc 1
 881
 Thr Asp Asp Ala Pro Leu
 600

cactcatttc tagtccagc 1
 900

<210> 4
 <211> 602
 <212> PRT
 <213> Human

<400> 4
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 20 25 30
 Asn Tyr Leu Thr Glu Asn Pro His Lys Lys Ala Asp Met Arg Arg Gln
 35 40 45
 Asp Ser Arg Gly Asn Thr Val Leu His Ala Leu Val Ala Ile Ala Asp
 50 55 60
 Asn Thr Arg Glu Asn Thr Lys Phe Val Thr Lys Met Tyr Asp Leu Leu
 65 70 75 80
 Leu Leu Lys Cys Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val
 85 90 95
 Leu Asn Asn Asp Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly
 100 105 110
 Lys Ile Gly Ile Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu
 115 120 125
 Asp Thr Arg His Leu Ser Arg Lys Phe Lys Asp Trp Ala Tyr Gly Pro
 130 135 140
 Val Tyr Ser Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu
 145 150 155 160
 Glu Ala Ser Val Leu Glu Ile Leu Val Tyr Asn Ser Lys Ile Glu Asn
 165 170 175
 Arg His Glu Met Leu Ala Val Glu Pro Ile Asn Glu Leu Leu Arg Asp
 180 185 190
 Lys Trp Arg Lys Phe Gly Ala Val Ser Phe Tyr Ile Asn Val Val Ser
 195 200 205
 Tyr Leu Cys Ala Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro
 210 215 220
 Leu Glu Gly Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu
 225 230 235 240
 Arg Leu Ala Gly Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe

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Sub
A2
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